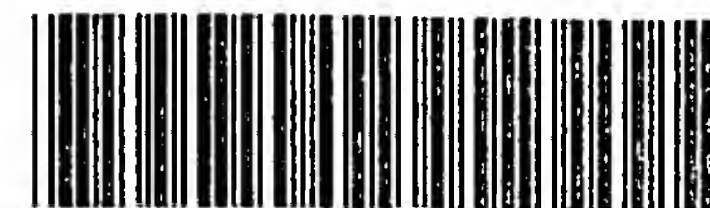


## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/591,419  
Source: IFWP  
Date Processed by STIC: 09/13/2006

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IFWP

## RAW SEQUENCE LISTING

DATE: 09/13/2006

PATENT APPLICATION: US/10/591,419

TIME: 13:09:30

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Output Set: N:\CRF4\09132006\J591419.raw

3 <110> APPLICANT: Frohberg, Claus  
 4 Koetting, Oliver  
 5 Ritte, Gerhard  
 6 Steup, Martin  
 8 <120> TITLE OF INVENTION: Methods for identifying proteins with starch phosphorylating enzymatic activity  
 9 activity  
 11 <130> FILE REFERENCE: 65084.000020  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/591,419  
 14 <141> CURRENT FILING DATE: 2006-09-01  
 16 <150> PRIOR APPLICATION NUMBER: PCT/EP2005/002454  
 17 <151> PRIOR FILING DATE: 2005-03-04  
 19 <150> PRIOR APPLICATION NUMBER: EP04090483.1  
 20 <151> PRIOR FILING DATE: 2004-12-15  
 22 <150> PRIOR APPLICATION NUMBER: EP04090121.7  
 23 <151> PRIOR FILING DATE: 2004-03-29  
 25 <150> PRIOR APPLICATION NUMBER: EP04090087.0  
 26 <151> PRIOR FILING DATE: 2004-03-05  
 28 <150> PRIOR APPLICATION NUMBER: US60/549,980 provisional  
 29 <151> PRIOR FILING DATE: 2004-03-05  
 31 <160> NUMBER OF SEQ ID NOS: 46  
 33 <170> SOFTWARE: PatentIn version 3.1  
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 37 <212> TYPE: DNA  
 38 <213> ORGANISM: Arabidopsis thaliana  
 40 <220> FEATURE:  
 41 <221> NAME/KEY: CDS  
 42 <222> LOCATION: (1)..(3591)  
 43 <223> OTHER INFORMATION:  
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 51 act aga aac tca tca tca tca ctt cct aga ctc gtt aac atc act cac 96  
 52 Thr Arg Asn Ser Ser Ser Ser Leu Pro Arg Leu Val Asn Ile Thr His  
 53 20 25 30  
 55 aga gtt aat ctc agc cac caa tct cac cga ctc aga aac tcc aat tct 144  
 56 Arg Val Asn Leu Ser His Gln Ser His Arg Leu Arg Asn Ser Asn Ser  
 57 35 40 45  
 59 cgt ctc act tgc act gct act tct tct tcc acc att gag gaa caa cgg 192  
 60 Arg Leu Thr Cys Thr Ala Thr Ser Ser Ser Thr Ile Glu Glu Gln Arg  
 61 50 55 60  
 63 aag aag aaa gat gga tca gga acg aaa gtg agg ttg aat gtg agg tta 240

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67	gat	cat	caa	gtt	aat	ttt	ggt	gac	cat	gtg	gct	atg	ttt	gga	tca	gct	288
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71	aaa	gag	att	ggt	tca	tgg	aaa	aag	aaa	tcg	cct	ttg	aat	tgg	agt	gag	336
72	Lys	Glu	Ile	Gly	Ser	Trp	Lys	Lys	Lys	Ser	Pro	Leu	Asn	Trp	Ser	Glu	
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75	aat	gga	tgg	gtt	tgt	gag	ttg	gaa	ctt	gac	ggt	ggt	cag	gtt	ttg	gag	384
76	Asn	Gly	Trp	Val	Cys	Glu	Leu	Glu	Leu	Asp	Gly	Gly	Gln	Val	Leu	Glu	
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79	tat	aag	ttt	gtc	att	gtt	aag	aat	gat	ggt	tca	ctt	tca	tgg	gaa	tct	432
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93			180					185					190				
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96	His	Asp	Val	Gly	Asp	Asp	Arg	Val	Val	Gly	Ser	Glu	Asn	Gly	Ala	Gln	
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107	gat	act	agt	ggt	ctt	gaa	ggc	aca	gct	ctt	aag	atg	gtt	gag	ggt	gat	768
108	Asp	Thr	Ser	Gly	Leu	Glu	Gly	Thr	Ala	Leu	Lys	Met	Val	Glu	Gly	Asp	
109				245						250				255			
111	cgc	aac	tct	aag	aac	tgg	tgg	aga	aag	ctt	gaa	atg	gta	cgc	gag	gtt	816
112	Arg	Asn	Ser	Lys	Asn	Trp	Trp	Arg	Lys	Leu	Glu	Met	Val	Arg	Glu	Val	
113				260					265					270			
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116	Ile	Val	Gly	Ser	Val	Glu	Arg	Glu	Glu	Arg	Leu	Lys	Ala	Leu	Ile	Tyr	
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119	tct	gca	att	tat	ttg	aag	tgg	ata	aac	aca	ggt	cag	att	cct	tgt	ttt	912
120	Ser	Ala	Ile	Tyr	Leu	Lys	Trp	Ile	Asn	Thr	Gly	Gln	Ile	Pro	Cys	Phe	
121		290					295					300					
123	gaa	gat	gga	ggg	cat	cac	cgt	cca	aac	agg	cat	gcc	gag	att	tcc	aga	960
124	Glu	Asp	Gly	Gly	His	His	Arg	Pro	Asn	Arg	His	Ala	Glu	Ile	Ser	Arg	
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127	ctt	ata	ttc	cgt	gag	ttg	gag	cac	att	tgc	agt	aag	aaa	gat	gct	act	1008
128	Leu	Ile	Phe	Arg	Glu	Leu	Glu	His	Ile	Cys	Ser	Lys	Lys	Asp	Ala	Thr	

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132	Pro Glu Glu Val Leu Val Ala Arg Lys Ile His Pro Cys Leu Pro Ser						
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135	ttc aaa gca gag ttt act gca gct gtc cct cta act cgg att agg gac						1104
136	Phe Lys Ala Glu Phe Thr Ala Ala Val Pro Leu Thr Arg Ile Arg Asp						
137		355		360		365	
139	ata gcc cat cgg aat gat att cct cat gat ctc aag caa gaa atc aag						1152
140	Ile Ala His Arg Asn Asp Ile Pro His Asp Leu Lys Gln Glu Ile Lys						
141		370		375		380	
143	cat acg ata caa aat aag ctt cac cgg aat gct ggt cca gaa gat cta						1200
144	His Thr Ile Gln Asn Lys Leu His Arg Asn Ala Gly Pro Glu Asp Leu						
145	385		390		395	400	
147	att gca aca gaa gca atg ctt caa cga att acc gag acc cca gga aaa						1248
148	Ile Ala Thr Glu Ala Met Leu Gln Arg Ile Thr Glu Thr Pro Gly Lys						
149		405		410		415	
151	tat agt gga gac ttt gtg gag cag ttt aaa ata ttc cat aat gag ctt						1296
152	Tyr Ser Gly Asp Phe Val Glu Gln Phe Lys Ile Phe His Asn Glu Leu						
153		420		425		430	
155	aaa gat ttc ttt aat gct gga agt ctc act gaa cag ctt gat tct atg						1344
156	Lys Asp Phe Phe Asn Ala Gly Ser Leu Thr Glu Gln Leu Asp Ser Met						
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159	aaa att tct atg gat gat aga ggt ctt tct gcg ctc aat ttg ttt ttt						1392
160	Lys Ile Ser Met Asp Asp Arg Gly Leu Ser Ala Leu Asn Leu Phe Phe						
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163	gaa tgt aaa aag cgc ctt gac aca tca gga gaa tca agc aat gtt ttg						1440
164	Glu Cys Lys Lys Arg Leu Asp Thr Ser Gly Glu Ser Ser Asn Val Leu						
165	465		470		475	480	
167	gag ttg att aaa acc atg cat tct cta gct tct tta aga gaa aca att						1488
168	Glu Leu Ile Lys Thr Met His Ser Leu Ala Ser Leu Arg Glu Thr Ile						
169		485		490		495	
171	ata aag gaa ctt aat agc ggc ttg cga aat gat gct cct gat act gcc						1536
172	Ile Lys Glu Leu Asn Ser Gly Leu Arg Asn Asp Ala Pro Asp Thr Ala						
173		500		505		510	
175	att gca atg cgc cag aag tgg cgc ctt tgt gag atc ggc ctc gag gac						1584
176	Ile Ala Met Arg Gln Lys Trp Arg Leu Cys Glu Ile Gly Leu Glu Asp						
177		515		520		525	
179	tac ttt ttt gtt cta cta agc aga ttc ctc aat gct ctt gaa act atg						1632
180	Tyr Phe Phe Val Leu Leu Ser Arg Phe Leu Asn Ala Leu Glu Thr Met						
181		530		535		540	
183	gga gga gct gat caa ctg gca aaa gat gtg gga tca aga aac gtt gcc						1680
184	Gly Gly Ala Asp Gln Leu Ala Lys Asp Val Gly Ser Arg Asn Val Ala						
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187	tca tgg aat gat cca cta gat gct ttg gtg ttg ggt gtt cac caa gta						1728
188	Ser Trp Asn Asp Pro Leu Asp Ala Leu Val Leu Gly Val His Gln Val						
189		565		570		575	
191	ggt cta tct ggt tgg aag caa gaa gaa tgt tta gcc att gga aat gaa						1776
192	Gly Leu Ser Gly Trp Lys Gln Glu Glu Cys Leu Ala Ile Gly Asn Glu						
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200	Asp	Gly	Lys	Thr	Ile	Trp	Ala	Met	Arg	Leu	Lys	Ala	Thr	Leu	Asp	Arg	
201		610					615					620					
203	gca	cgc	aga	tta	aca	gca	gaa	tat	tct	gat	ttg	ctt	ctt	caa	ata	ttt	1920
204	Ala	Arg	Arg	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	Leu	Leu	Leu	Gln	Ile	Phe	
205	625					630					635					640	
207	cct	cct	aat	gtg	gag	att	tta	gga	aaa	gct	cta	gga	att	cca	gag	aat	1968
208	Pro	Pro	Asn	Val	Glu	Ile	Leu	Gly	Lys	Ala	Leu	Gly	Ile	Pro	Glu	Asn	
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211	agt	gtc	aag	acc	tat	aca	gaa	gca	gag	att	cgt	gct	gga	att	att	ttc	2016
212	Ser	Val	Lys	Thr	Tyr	Thr	Glu	Ala	Glu	Ile	Arg	Ala	Gly	Ile	Ile	Phe	
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220	Leu	Gly	Ser	Glu	Gly	Trp	Asp	Val	Val	Val	Pro	Gly	Ser	Thr	Ser	Gly	
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224	Thr	Leu	Val	Gln	Val	Glu	Ser	Ile	Val	Pro	Gly	Ser	Leu	Pro	Ala	Thr	
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233				740					745					750			
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236	Glu	Leu	Pro	His	Leu	Ser	His	Leu	Gly	Val	Arg	Ala	Arg	Gln	Glu	Lys	
237			755					760					765				
239	att	gtc	ttt	gtg	aca	tgt	gat	gat	gat	gac	aag	gtt	gct	gat	ata	cga	2352
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241		770					775						780				
243	cga	ctt	gtg	gga	aaa	ttt	gtg	agg	ttg	gaa	gca	tct	cca	agt	cat	gtg	2400
244	Arg	Leu	Val	Gly	Lys	Phe	Val	Arg	Leu	Glu	Ala	Ser	Pro	Ser	His	Val	
245	785					790					795					800	
247	aat	ctg	ata	ctt	tca	act	gag	ggt	agg	agt	cgc	act	tcc	aaa	tcc	agt	2448
248	Asn	Leu	Ile	Leu	Ser	Thr	Glu	Gly	Arg	Ser	Arg	Thr	Ser	Lys	Ser	Ser	
249				805						810					815		
251	gcg	acc	aaa	aaa	acg	gat	aag	aac	agc	tta	tct	aag	aaa	aaa	aca	gat	2496
252	Ala	Thr	Lys	Lys	Thr	Asp	Lys	Asn	Ser	Leu	Ser	Lys	Lys	Lys	Thr	Asp	
253				820					825					830			
255	aag	aag	agc	tta	tct	atc	gat	gat	gaa	gaa	tca	aag	cct	ggt	tcc	tca	2544
256	Lys	Lys	Ser	Leu	Ser	Ile	Asp	Asp	Glu	Glu	Ser	Lys	Pro	Gly	Ser	Ser	
257			835					840					845				
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264	Ile	Ile	Ala	Leu	Ala	Asp	Ala	Asp	Val	Pro	Thr	Ser	Gly	Ser	Lys	Ser	
265	865						870				875					880	
267	gct	gca	tgt	ggt	ctt	ctt	gca	tct	tta	gca	gaa	gcc	tct	agt	aaa	gtg	2688
268	Ala	Ala	Cys	Gly	Leu	Leu	Ala	Ser	Leu	Ala	Glu	Ala	Ser	Ser	Lys	Val	
269					885					890					895		
271	cac	agc	gaa	cac	gga	gtt	ccg	gca	tca	ttt	aag	gtt	cca	act	gga	gtt	2736
272	His	Ser	Glu	His	Gly	Val	Pro	Ala	Ser	Phe	Lys	Val	Pro	Thr	Gly	Val	
273				900					905				910				
275	gtc	ata	cct	ttt	gga	tcg	atg	gaa	tta	gct	tta	aag	caa	aat	aat	tcg	2784
276	Val	Ile	Pro	Phe	Gly	Ser	Met	Glu	Leu	Ala	Leu	Lys	Gln	Asn	Asn	Ser	
277			915					920					925				
279	gaa	gaa	aag	ttt	gcg	tct	ttg	cta	gaa	aaa	cta	gaa	acc	gcc	aga	cct	2832
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287	aaa	acg	ttg	caa	gtg	cct	aaa	gaa	aca	atc	aac	agc	ata	agc	aaa	gcg	2928
288	Lys	Thr	Leu	Gln	Val	Pro	Lys	Glu	Thr	Ile	Asn	Ser	Ile	Ser	Lys	Ala	
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292	Phe	Leu	Lys	Asp	Ala	Arg	Leu	Ile	Val	Arg	Ser	Ser	Ala	Asn	Val	Glu	
293			980						985					990			
295	gac	tta	gcc	gga	atg	tca	gct	gca	gga	ctc	tat	gaa	tca	atc	cct	aac	3024
296	Asp	Leu	Ala	Gly	Met	Ser	Ala	Ala	Gly	Leu	Tyr	Glu	Ser	Ile	Pro	Asn	
297		995					1000						1005				
299	gtg	agt	ccc	tcg	gat	cct	ttg	gtg	ttt	tca	gat	tcg	gtt	tgc	caa		3069
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308	Ala	Ala	Gly	Val	Ser	Gln	Arg	Glu	Ala	Ser	Met	Ala	Val	Leu	Val		
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311	caa	gaa	atg	ctt	tcg	ccg	gac	tta	tca	ttc	gtt	ctg	cac	aca	gtg		3204
312	Gln	Glu	Met	Leu	Ser	Pro	Asp	Leu	Ser	Phe	Val	Leu	His	Thr	Val		
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316	Ser	Pro	Ala	Asp	Pro	Asp	Ser	Asn	Leu	Val	Glu	Ala	Glu	Ile	Ala		
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321		1085					1090						1095				
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/591,419

DATE: 09/13/2006

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